AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1. (Currently Amended) A method for analyzing expression levels of exon variants of a plurality of different genes in the genome of an organism in a cell sample derived from said organism, said method comprising measuring, *in vitro*, the nucleic acid expression levels of a plurality of different variants of an exon of a gene, for each gene in said plurality of different genes in the genome of said organism from said cell sample, each of said different variants being a different splice form of said exon generated using a different 3′ or 5′ splice junction of said exon; and wherein said measuring step is performed by a method comprising:

(a) contacting a positionally-addressable array of polynucleotide probes with a nucleic acid sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, wherein said plurality of polynucleotide probes comprises a probe that specifically hybridizes to one of said different variants of an exon of a gene, for each gene in said plurality of different genes; and

(b) measuring levels of hybridization between said plurality of polynucleotide probes and said RNAs or said nucleic acids, wherein said levels of hybridization indicate the nucleic acid expression levels of said plurality of different variants;

thereby analyzing the expression levels of said exon variants.

2-6 (Canceled).

7. (Previously Presented) The method of claim 1, wherein said plurality of different genes consists of at least 100 different genes.

8. (Previously Presented) The method of claim 1, wherein said plurality of different genes consists of at least 1,000 different genes.

9. (Previously Presented) The method of claim 1, wherein said plurality of different genes consists of at least 10,000 different genes.

10-13. (Canceled)

14. (Previously Presented) The method of claim 1, wherein said plurality of polynucleotide probes consists of at least 100 different polynucleotide probes.

15. (Previously Presented) The method of claim 1, wherein said plurality of polynucleotide probes consists of at least 1,000 different polynucleotide probes.

16. (Previously Presented) The method of claim 1, wherein said plurality of polynucleotide probes consists of at least 10,000 different polynucleotide probes.

17. (Previously Presented) The method of claim 1, wherein said plurality of polynucleotide probes is in the range of 1,000 to 50,000 different polynucleotide probes.

18. (Previously Presented) The method of claim 1, wherein said positionally-addressable array has in the range of 100 to 1,000 different polynucleotide probes per 1 cm^2.

19. (Previously Presented) The method of claim 1, wherein said positionally-addressable array has in the range of 1,000 to 10,000 different polynucleotide probes per 1 cm^2.

20. (Previously Presented) The method of claim 1, wherein said positionally-addressable array has in the range of 10,000 to 50,000 different polynucleotide probes per 1 cm^2.

21. (Previously Presented) The method of claim 1, wherein said positionally-addressable array has more than 50,000 different polynucleotide probes per 1 cm^2.

22. (Previously Presented) The method of claim 1, wherein each of said different nucleotide sequences consists of 10 to 1,000 nucleotides.

23. (Previously Presented) The method of claim 1, wherein each of said different nucleotide sequences consists of 15 to 600 nucleotides.

24. (Previously Presented) The method of claim 1, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

25. (Previously Presented) The method of claim 1, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

26. (Previously Presented) The method of claim 1, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

27. (Previously Presented) The method of claim 1, wherein each of said different nucleotide sequences consists of 60 nucleotides.

28. (Previously Presented) The method of claim 1, wherein at least one probe in said plurality of polynucleotide probes comprises a linker sequence.

29. (Canceled)

30. (Canceled)

31. (Previously Presented) The method of claim 1, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a multiexon in a gene in the genome of said organism.

32. (Previously Presented) The method of claim 31, wherein the nucleotide sequence of said at least one polynucleotide probe is complementary to a sequence spanning the splice junction between different exons in said multiexon.

33. (Previously Presented) The method of claim 31, wherein said sequence is complementary to a sequence comprising a full length exon flanked by sequences from an adjacent exon or exons in said multiexon.

34. (Previously Presented) The method of claim 1, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences

complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

35. (Canceled).

36. (Previously Presented) The method of claim 1, wherein said nucleic acid expression levels are measured as abundance of mRNA transcripts.

37-44. (Canceled).

45. (Previously Presented) The method of claim 1, wherein said organism is a human.

46. (Withdrawn) The method of claim 1, wherein said organism is a plant.

47-85. (Canceled).

86. (Previously Presented) The method of claim 1, wherein said cell sample has been subjected to a perturbation.

87. (Previously Presented) The method of claim 86, wherein said organism is a human.

88. (Withdrawn) The method of claim 86, wherein said organism is a plant.

89. (Previously Presented) The method of claim 86, further comprising comparing the nucleic acid expression levels of at least a portion of said plurality of different variants in said nucleic acid sample derived from said cell sample subjected to said perturbation with the nucleic acid expression levels of said at least portion of said plurality of different variants in a second nucleic acid sample derived from a cell sample of the same type not subjected to said perturbation.

90. (Previously Presented) The method of claim 89, wherein said comparing comprises determining the difference between the nucleic acid expression levels of each variant in said at least portion of said plurality of different variants in said nucleic acid sample derived from said cell sample subjected to said perturbation and the nucleic acid expression levels of the

corresponding variants in said second nucleic acid sample derived from a cell sample of the same type not subjected to said perturbation.

91-211 (Canceled).

212. (Withdrawn) The method of claim 1, wherein said organism is a fungus.

213. (Withdrawn) The method of claim 86, wherein said organism is a fungus.

214-262 (Canceled).

263. (Previously Presented) The method of claim 1, wherein said array of polynucleotide probes comprises one or more sets of successive overlapping probes tiled along the longest length variant among said plurality of different variants of said exon.

264. (Previously Presented) The method of claim 1, wherein said array of polynucleotide probes comprises variant junction probes, wherein each of said variant junction probes is specifically hybridizable to a sequence spanning the splice junction between a different one of said plurality of different variants of said exon and an adjacent exon.

265. (Previously Presented) The method of claim 86, wherein said perturbation is exposure to a drug.

266. (Withdrawn) The method of claim 86, wherein said perturbation is a genetic mutation.

267. (Withdrawn) The method of claim 86, wherein said perturbation comprises mutation of one or more genes and exposure to a drug.

268-279 (Canceled).

280. (Previously Presented) The method of any one of claims 32, 263, and 264 wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

281. (Previously Presented) The method of claim 280, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

282. (Previously Presented) The method of claim 281, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

283. (Previously Presented) The method of claim 282, wherein each of said different nucleotide sequences consists of 60 nucleotides.

284. (Currently Amended) A method for analyzing expression levels of exon variants of a plurality of different genes in the genome of an organism in a cell sample derived from said organism, said method comprising:

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises (i) one or more exon specific probes comprising different nucleotide sequences for each of a plurality of different genes in the genome of said organism, wherein each of said different nucleotide sequences is complementary and hybridizes to a sequence within a different individual exon; and (ii) a variant junction probe for each of a plurality of different variants of at least one exon for each gene in said plurality of different genes, each of said different variants being a different splice form of said exon generated using a different 3′ or 5′ splice junction of said exon, and each of said variant junction probes being a probe specific to a junction region of said variant and an adjacent exon in a multiexon comprising said variant of said exon, each of said exon specific probes and variant junction probes being bound to a different region of a support; and

(b) measuring levels of hybridization (i) between each of said exon specific probes and said RNAs or said nucleic acids, and (ii) between each of said variant junction probes and said RNAs or said nucleic acids, wherein said levels of hybridization indicate the nucleic acid expression levels of said plurality of different variants,

thereby analyzing the expression levels of said exon variants.

285. (Currently Amended) A method for analyzing expression levels of exon variants of a plurality of different genes in the genome of an organism in a cell sample derived from said organism, said method comprising:

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of junction specific probes comprising different nucleotide sequences for each of a plurality of different genes in the genome of said organism bound to different regions of a support, wherein each of said different nucleotide sequences is complementary and hybridizes to a sequence spanning a junction region of a multiexon in a gene of the genome of said organism, and wherein said plurality of junction specific probes comprises a variant junction probe for each of a plurality of different variants of at least one exon for each gene in said plurality of different genes, each of said different variants being a different splice form of said exon generated using a different 3′ or 5′ splice junction of said exon, and each of said variant junction probes being a probe specific to a junction region of said variant and an adjacent exon in a multiexon comprising said variant of said exon; and

(b) measuring levels of hybridization between said plurality of junction probes and said RNAs or said nucleic acids, wherein said levels of hybridization indicate the nucleic acid expression levels of said plurality of different variants,

thereby analyzing the expression levels of said exon variants.

286. (Previously Presented) The method of claim 284 or 285, wherein said plurality of different genes consists of at least 100 different genes.

287. (Previously Presented) The method of claim 286, wherein said plurality of different genes consists of at least 1,000 different genes.

288. (Previously Presented) The method of claim 287, wherein said plurality of different genes consists of at least 10,000 different genes.

289. (Previously Presented) The method of claim 284 or 285, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

290. (Previously Presented) The method of claim 289, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

291. (Previously Presented) The method of claim 290, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

292. (Previously Presented) The method of claim 291, wherein each of said different nucleotide sequences consists of 60 nucleotides.

293. (Currently Amended) The method of claim 1, wherein said method comprises measuring, *in vitro*, the nucleic acid expression levels of at least 5 of said different variants of ~~an~~ said exon.

294. (Currently Amended) The method of claim 293, wherein said method comprises measuring, *in vitro*, the nucleic acid expression levels of at least 10 of said different variants of ~~an~~ said exon.

295. (Currently Amended) The method of claim 294, wherein said method comprises measuring, *in vitro*, the nucleic acid expression levels of at least 100 of said different variants of ~~an~~ said exon.

296. (Currently Amended) The method of claim 295, wherein said method comprises measuring, *in vitro*, the nucleic acid expression levels of at least 1000 of said different variants of ~~an~~ said exon.